

O I P E
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PENT & TRADEMA

SEQUENCE LISTING

<110> VisiGen Biotechnologies, Inc.

<120> REAL-TIME SEQUENCE DETERMINATION

<130> 00007/01PCT

<140> PCT/US01/21811

<141> 2001-07-09

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<151> 2000-07-07

<160> 57

<170> PatentIn version 3.1

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<211> 19

<212> DNA

<213> Artificial

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<223> Primer strand used to test incorporation of gamma-tagged dNTPs using Taq DNA Polymerase I.

<220>

<221> Primer

<222> (1)..(19)

<223> 5' to 3' primer strand called TOP

<400> 1

ggtaactaagc ggccgcata

19

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<223> Templates strand used to test incorporation of gamma-tagged dNTPs using Taq DNA Polymerase I.

<220>

<221> Template
<222> (1)..(21)
<223> 3' to 5' template strand BOT-T

<400> 2
ccatgattcg ccggcgtact c
21

<210> 3
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<213> Artificial

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using Taq DNA Polymerase I.

<220>
<221> Template
<222> (1)..(21)
<223> 3' to 5' template strand called BOT-C

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ccatgattcg ccggcgtacc c
21

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<213> Artificial

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using Taq DNA Polymerase I.

<220>
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<222> (1)..(21)
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ccatgattcg ccggcgtacg c
21

<210> 5
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using Taq DNA Polymerase I.

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<223> 3' to 5' template strand called BOT-A

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21

<210> 6
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using Taq DNA Polymerase I.

<220>
<221> Template
<222> (1)..(23)
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<400> 6
ccatgattcg ccggcgtact ttc
23

<210> 7
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<213> Artificial

<220>
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dNTPs
using Taq DNA Polymerase I.

<220>
<221> Template
<222> (1)..(23)
<223> 3' to 5' template strand called BOT-Sau

<400> 7
ccatgattcg ccggcgtaacc tag
23

<210> 8
<211> 38
<212> DNA
<213> *Thermus aquaticus*

<220>
<221> primer_bind
<222> (1)..(38)
<223> TAQ forward primer

<400> 8
gcgaattcat gagggggatg ctgcccctct ttgagccc
38

<210> 9
<211> 37
<212> DNA
<213> *Thermus aquaticus*

<220>
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<222> (1)..(37)
<223> TAQ Pol I Reverse Primer

<400> 9
gcgaattcac cctccttggc ggagcgccag tcctccc
37

<210> 10
<211> 37
<212> DNA
<213> *Thermus aquaticus*

<220>
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<222> (1)..(37)
<223> Taq Pol I A293 Trunk

<400> 10
aatccatggg ccctggagga ggcccccctgg cccccgc
37

<210> 11
<211> 832
<212> PRT
<213> Thermus aquaticus

<400> 11

Met Arg Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu
1 5 10 15

Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys Gly
20 25 30

Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala
35 40 45

Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile Val
50 55 60

Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly Gly
65 70 75 80

Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu
85 90 95

Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu Glu
100 105 110

Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys Lys
115 120 125

Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys Asp
130 135 140

Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu Gly
145 150 155 160

Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg Pro
165 170 175

Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp Asn
180 185 190

Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu Leu
195 200 205

Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg Leu
210 215 220

Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu Lys
225 230 235 240

Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu Val
245 250 255

Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala Phe
260 265 270

Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu
275 280 285

Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly
290 295 300

Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala Asp
305 310 315 320

Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala Pro
325 330 335

Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu Leu
340 345 350

Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu Pro
355 360 365

Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn
370 375 380

Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu
385 390 395 400

Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn Leu
405 410 415

Trp Gly Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg Glu
420 425 430

Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr Gly
435 440 445

Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val Ala
450 455 460

Glu Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly His
465 470 475 480

Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp
485 490 495

Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys Arg
500 505 510

Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile
515 520 525

Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser Thr

530 535 540

Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg Leu
545 550 555 560

His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser
565 570 575

Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln
580 585 590

Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val Ala
595 600 605

Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly
610 615 620

Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His Thr
625 630 635 640

Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp Pro
645 650 655

Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr Gly
660 665 670

Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu Glu
675 680 685

Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg
690 695 700

Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr Val
705 710 715 720

Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala Arg
725 730 735

Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro
740 745 750

Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu
755 760 765

Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val His
770 775 780

Asp Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val Ala
785 790 795 800

Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val Pro
805 810 815

Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys Glu
820 825 830

<210> 12
<211> 19
<212> PRT
<213> *Thermus aquaticus*

<220>
<221> MISC_FEATURE
<222> (2)..(4)
<223> Residues in native protein are Ser Trp Met

<220>
<221> MISC_FEATURE
<222> (6)..(6)
<223> Residue in native protein is Gly

<220>
<221> MISC_FEATURE
<222> (8)..(9)
<223> Residues in native protein are Pro Arg

<400> 12

Ala Xaa Xaa Xaa Phe Xaa Val Xaa Xaa Glu Ala Val Asp Pro Leu Met

1

5

10

15

Arg Arg Ala

<210> 13
<211> 32
<212> DNA
<213> *Thermus aquaticus*

<220>
<221> mutation
<222> (14)..(15)
<223> Residue 643 Ala to Cys mutation forward primer: Codon GCC
mutated to TGC

<400> 13
ccacacggag acctgcagct ggatgttcgg cg
32

<210> 14
<211> 32
<212> DNA
<213> *Thermus aquaticus*

<220>
<221> mutation
<222> (18)..(18)
<223> Residue 643 Ala to Cys mutation reverse primer: antisense
Codon GGC mutated to
GCA

<400> 14
cgccgaacat ccacgagcag gtctccgtgt gg
32

<210> 15
<211> 35
<212> DNA
<213> *Thermus aquaticus*

<220>
<221> mutation
<222> (16)..(16)

<223> Residue 647 Phe to Cys mutation forward primer: Codon ttc mutated to tgc

<400> 15
ccggccagctg gatgtgcggc gtccccggg aggcc
35

<210> 16
<211> 35
<212> DNA
<213> *Thermus aquaticus*

<220>
<221> mutation
<222> (20)..(20)
<223> Residue 647 Phe to Cys mutation reverse primer: antisense Codon gAa mutated to
gCa

<400> 16
ggcctcccg gggacgcccgc acatccacgt ggcgg
35

<210> 17
<211> 37
<212> DNA
<213> *Thermus aquaticus*

<220>
<221> mutation
<222> (19)..(20)
<223> Residue 649 Val to Cys mutation forward primer: Codon gtc mutated to tgc

<400> 17
gccagctgga tgttcggctg ccccccggag gccgtgg
37

<210> 18
<211> 37
<212> DNA
<213> *Thermus aquaticus*

<220>

<221> mutation
<222> (18)..(19)
<223> Residue 649 Val to Cys mutation reverse primer: antisense
Codon gAC mutated to
gCA

<400> 18
ccacggcctc ccggggcag ccgaacatcc agctggc
37

<210> 19
<211> 36
<212> DNA
<213> *Thermus aquaticus*

<220>
<221> mutation
<222> (13)..(15)
<223> Residue 652 Glu to Cys mutation forward primer: Codon
gag mutated to tgc

<400> 19
ggcgtccccc ggtgcgcgt ggacccctg atgcgc
36

<210> 20
<211> 36
<212> DNA
<213> *Thermus aquaticus*

<220>
<221> mutation
<222> (22)..(24)
<223> Residue 652 Glu to Cys mutation reverse primer: antisense
Codon CTC mutated to
GCA

<400> 20
gcgcatcagg gggtccacgg cgcacccggg gacgcc
36

<210> 21
<211> 36
<212> DNA

<213> *Thermus aquaticus*

<220>

<221> mutation

<222> (16)..(17)

<223> Residue 653 Ala to Cys mutation forward primer: Codon gcc mutated to tgc

<400> 21
ggcgtccccc gggagtgcgt ggacccctg atgcgc
36

<210> 22

<211> 36

<212> DNA

<213> *Thermus aquaticus*

<220>

<221> mutation

<222> (20)..(21)

<223> Residue 653 Ala to Cys mutation reverse primer: antisense Codon gGC mutated to
gCA

<400> 22
gcgcatcagg gggtccacgc actccgggg gacgcc
36

<210> 23

<211> 33

<212> DNA

<213> *Thermus aquaticus*

<220>

<221> mutation

<222> (16)..(18)

<223> Residue 654 Val to Cys mutation forward primer: Codon gtg mutated to tgt

<400> 23
gtccccccggg aggccctgtga cccctgatg cgc
33

<210> 24

<211> 33
<212> DNA
<213> *Thermus aquaticus*

<220>
<221> mutation
<222> (16)..(18)
<223> Residue 654 Val to Cys mutation reverse primer: antisense
Codon CAC mutated to
ACA

<400> 24
gctccatcagg gggcacagg cctccgggg gac
33

<210> 25
<211> 33
<212> DNA
<213> *Thermus aquaticus*

<220>
<221> mutation
<222> (16)..(17)
<223> Residue 655 Asp to Cys mutation forward primer: Codon
gac mutated to tgc

<400> 25
ccccgggagg ccgtgtgcc cctgatgcgc cg
33

<210> 26
<211> 33
<212> DNA
<213> *Thermus aquaticus*

<220>
<221> mutation
<222> (17)..(18)
<223> Residue 655 Asp to Cys mutation reverse primer: antisense
Codon gTC mutated to
gCA

<400> 26
ccggcgcatc agggggcaca cggcctcccg ggg
33

<210> 27

<211> 33

<212> DNA

<213> *Thermus aquaticus*

<220>

<221> mutation

<222> (16)..(17)

<223> Residue 656 Pro to Cys mutation reverse primer: Codon
ccc mutated to tgc

<400> 27

cgggaggccg tggactgcct gatgcgccgg gcg

33

<210> 28

<211> 33

<212> DNA

<213> *Thermus aquaticus*

<220>

<221> mutation

<222> (17)..(18)

<223> Residue 656 Pro to Cys mutation reverse primer: antisense
Codon gGG mutated to
gCA

<400> 28

cgtccggcgatcaggcagt ccacggcctc ccg

33

<210> 29

<211> 30

<212> DNA

<213> *Thermus aquaticus*

<220>

<221> mutation

<222> (13)..(15)

<223> Residue 657 Leu to Cys mutation forward primer: Codon
ctg mutated to tgc

<400> 29

gccgtggacc cctgcattgcg ccggggggcc

30

<210> 30
<211> 30
<212> DNA
<213> Thermus aquaticus

<220>
<221> mutation
<222> (16)..(18)
<223> Residue 657 Leu to Cys mutation reverse primer: antisense
Codon CAG mutated to
GCA

<400> 30
ggccgcccgg cgcatgcagg ggtccacggc
30

<210> 31
<211> 30
<212> DNA
<213> Thermus aquaticus

<220>
<221> mutation
<222> (16)..(18)
<223> Residue 658 Met to Cys mutation forward primer: Codon
atg mutated to tgc

<400> 31
gccgtggacc ccctgtgtcg ccgggcggcc
30

<210> 32
<211> 30
<212> DNA
<213> Thermus aquaticus

<220>
<221> mutation
<222> (13)..(15)
<223> Residue 658 Met to Cys mutation reverse primer: antisense
Codon CAT mutated to
ACA

<400> 32
ggccgccccgg cgacacaggg ggtccacggc
30

<210> 33
<211> 36
<212> DNA
<213> *Thermus aquaticus*

<220>
<221> mutation
<222> (19)..(19)
<223> Residue 659 Arg to Cys mutation forward primer: Codon
cgc mutated to tgc

<400> 33
gccgtggacc ccctgatgtg ccgggcggcc aagacc
36

<210> 34
<211> 36
<212> DNA
<213> *Thermus aquaticus*

<220>
<221> mutation
<222> (18)..(18)
<223> Residue 659 Arg to Cys mutation reverse primer: antisense
Codon gcG mutated to
gca

<400> 34
ggtcttggcc gcccggcaca tcagggggtc cacggc
36

<210> 35
<211> 33
<212> DNA
<213> *Thermus aquaticus*

<220>
<221> mutation
<222> (16)..(18)
<223> Residue 660 Arg to Cys mutation forward primer: Codon
cgg mutated to tgc

<400> 35
gaccggctga tgcgctgcgc ggccaagacc atc
33

<210> 36
<211> 33
<212> DNA
<213> *Thermus aquaticus*

<220>
<221> mutation
<222> (16)..(18)
<223> Residue 660 Arg to Cys mutation reverse primer: antisense
Codon CcG mutated to
GcA

<400> 36
gatggtcttg gccgcgcagc gcatcagggg gtc
33

<210> 37
<211> 33
<212> DNA
<213> *Thermus aquaticus*

<220>
<221> mutation
<222> (16)..(18)
<223> Residue 661 Ala to Cys mutation forward primer: Codon
gog mutated to tgc

<400> 37
cccctgatgc gccggtgcgca aagaccatc aac
33

<210> 38
<211> 33
<212> DNA
<213> *Thermus aquaticus*

<220>
<221> mutation
<222> (16)..(18)
<223> Residue 661 Ala to Cys mutation reverse primer: antisense

Codon CGC mutated to
GCA

<400> 38
gttgatggtc ttggcgacc ggcgcatcag ggg
33

<210> 39
<211> 19
<212> PRT
<213> *Thermus aquaticus*

<220>
<221> variant
<222> (1)..(1)
<223> Taq Pol I Residues 643 to 661; Residue 643 ala to cys
variant

<400> 39

Cys Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp Pro Leu Met
1 5 10 15

Arg Arg Ala

<210> 40
<211> 19
<212> PRT
<213> *Thermus aquaticus*

<220>
<221> variant
<222> (5)..(5)
<223> Taq Pol I Residues 643 to 661; Residue 647 phe to cys
variant

<400> 40

Ala Ser Trp Met Cys Gly Val Pro Arg Glu Ala Val Asp Pro Leu Met
1 5 10 15

Arg Arg Ala

<210> 41
<211> 19
<212> PRT
<213> *Thermus aquaticus*

<220>
<221> variant
<222> (7)..(7)
<223> Taq Pol I Residues 643 to 661; Residue 649 val to cys
variant

<400> 41

Ala Ser Trp Met Phe Gly Cys Pro Arg Glu Ala Val Asp Pro Leu Met
1 5 10 15

Arg Arg Ala

<210> 42
<211> 19
<212> PRT
<213> *Thermus aquaticus*

<220>
<221> variant
<222> (10)..(10)
<223> Taq Pol I Residues 643 to 661; Residue 652 glu to cys
variant

<400> 42

Ala Ser Trp Met Phe Gly Val Pro Arg Cys Ala Val Asp Pro Leu Met
1 5 10 15

Arg Arg Ala

<210> 43
<211> 19
<212> PRT

<213> *Thermus aquaticus*
<220>
<221> variant
<222> (11)..(11)
<223> Taq Pol I Residues 643 to 661; Residue 653 ala to cys
variant

<400> 43

Ala Ser Trp Met Phe Gly Val Pro Arg Glu Cys Val Asp Pro Leu Met
1 5 10 15

Arg Arg Ala

<210> 44
<211> 19
<212> PRT
<213> *Thermus aquaticus*
<220>
<221> variant
<222> (12)..(12)
<223> Taq Pol I Residues 643 to 661; Residue 654 val to cys
variant

<400> 44

Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Cys Asp Pro Leu Met
1 5 10 15

Arg Arg Ala

<210> 45
<211> 19
<212> PRT
<213> *Thermus aquaticus*
<220>
<221> variant
<222> (13)..(13)
<223> Taq Pol I Residues 643 to 661; Residue 655 asp to cys

variant

<400> 45

Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Cys Pro Leu Met
1 5 10 15

Arg Arg Ala

<210> 46

<211> 19

<212> PRT

<213> Thermus aquaticus

<220>

<221> variant

<222> (14)..(14)

<223> Taq Pol I Residues 643 to 661; Residue 656 pro to cys
variant

<400> 46

Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp Cys Leu Met
1 5 10 15

Arg Arg Ala

<210> 47

<211> 19

<212> PRT

<213> Thermus aquaticus

<220>

<221> variant

<222> (15)..(15)

<223> Taq Pol I Residues 643 to 661; Residue 657 leu to cys
variant

<400> 47

Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp Pro Cys Met

1

5

10

15

Arg Arg Ala

<210> 48
<211> 19
<212> PRT
<213> Thermus aquaticus

<220>
<221> variant
<222> (16)..(16)
<223> Taq Pol I Residues 643 to 661; Residue 658 met to cys
variant

<400> 48

Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp Pro Leu Cys
1 5 10 15

Arg Arg Ala

<210> 49
<211> 19
<212> PRT
<213> Thermus aquaticus

<220>
<221> variant
<222> (17)..(17)
<223> Taq Pol I Residues 643 to 661; Residue 659 arg to cys
variant

<400> 49

Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp Pro Leu Met
1 5 10 15

Cys Arg Ala

<210> 50
<211> 19
<212> PRT
<213> *Thermus aquaticus*

<220>
<221> variant
<222> (18)..(18)
<223> Taq Pol I Residues 643 to 661; Residue 660 arg to cys
variant

<400> 50

Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp Pro Leu Met
1 5 10 15

Arg Cys Ala

<210> 51
<211> 19
<212> PRT
<213> *Thermus aquaticus*

<220>
<221> variant
<222> (19)..(19)
<223> Taq Pol I Residues 643 to 661; Residue 661 ala to cys
variant

<400> 51

Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp Pro Leu Met
1 5 10 15

Arg Arg Cys

<210> 52
<211> 6
<212> PRT
<213> *Thermus aquaticus*

<220>

<221> variant
<222> (1)..(1)
<223> Taq Pol I Residues 513 to 518; Residue 513 ser to cys
variant

<400> 52

Cys Thr Ser Ala Ala Val
1 5

<210> 53
<211> 6
<212> PRT
<213> *Thermus aquaticus*

<220>
<221> variant
<222> (2)..(2)
<223> Taq Pol I Residues 513 to 518; Residue 514 thr to cys
variant

<400> 53

Ser Cys Ser Ala Ala Val
1 5

<210> 54
<211> 6
<212> PRT
<213> *Thermus aquaticus*

<220>
<221> variant
<222> (3)..(3)
<223> Taq Pol I Residues 513 to 518; Residue 515 ser to cys
variant

<400> 54

Ser Thr Cys Ala Ala Val
1 5

<210> 55
<211> 6

<212> PRT

<213> *Thermus aquaticus*

<220>

<221> variant

<222> (4)..(4)

<223> Taq Pol I Residues 513 to 518; Residue 515 ala to cys
variant

<400> 55

Ser Thr Ser Cys Ala Val

1 5

<210> 56

<211> 6

<212> PRT

<213> *Thermus aquaticus*

<220>

<221> variant

<222> (5)..(5)

<223> Taq Pol I Residues 513 to 518; Residue 517 ala to cys
variant

<400> 56

Ser Thr Ser Ala Cys Val

1 5

<210> 57

<211> 6

<212> PRT

<213> *Thermus aquaticus*

<220>

<221> variant

<222> (6)..(6)

<223> Taq Pol I Residues 513 to 518; Residue 518 val to cys
variant

<400> 57

Ser Thr Ser Ala Ala Cys

1 5